

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2003, 04:11:53 ; Search time 105 Seconds
(without alignment)
8508.185 Million cell updates/sec

Title: US-09-856-327-1_COPY_1_2024
Perfect score: 2024
Sequence: 1 atcagcagctctctctctca.....ttatggcactatgattcatg 2024

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 500186

Minimum DB seq length: 15

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/2/ina/5A-COMB.seq:*
 - 2: /cgn2_6/ptodata/2/ina/5B-COMB.seq:*
 - 3: /cgn2_6/ptodata/2/ina/5A-COMB.seq:*
 - 4: /cgn2_6/ptodata/2/ina/5B-COMB.seq:*
 - 5: /cgn2_6/ptodata/2/ina/5A-COMB.seq:*
 - 6: /cgn2_6/ptodata/2/ina/5B-COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
C 1	15	0.7	20 4	US-09-198-452A-1839
2	15	0.7	22 1	US-08-487-135B-10
3	15	0.7	22 2	US-08-915-972A-10
4	15	0.7	22 2	US-09-177-909-10
5	15	0.7	24 2	US-08-553-304-2
6	15	0.7	27 2	US-08-639-857-27
7	14	0.7	17 1	US-08-374-155A-23
8	14	0.7	17 2	US-08-785-396-23
9	14	0.7	17 4	US-08-584-040-6039
C 10	14	0.7	17 4	US-08-584-040-6040
C 11	14	0.7	17 4	US-09-371-772B-2876
C 12	14	0.7	17 4	US-09-371-772B-2877
C 13	14	0.7	20 2	US-08-044-506A-13
C 14	14	0.7	20 3	US-08-850-347-12
C 15	14	0.7	20 3	US-08-990-065-12
C 16	14	0.7	20 3	US-09-379-523-2
17	14	0.7	20 4	US-09-600-770A-29
18	14	0.7	20 4	US-09-422-978-8208
19	14	0.7	20 4	US-09-198-452A-5504
C 20	14	0.7	22 4	US-09-193-612B-21
C 21	14	0.7	23 4	US-09-328-571A-6
C 22	14	0.7	24 4	US-09-146-580-17
23	14	0.7	24 4	US-09-638-544-12
C 24	14	0.7	25 1	US-08-753-147-119
25	14	0.7	27 2	US-08-922-171-6
26	14	0.7	27 4	US-09-242-913B-6
C 27	13	0.6	15 4	US-09-346-551-4

C 28	13	0.6	15 4	US-10-001-344-4
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30	13	0.6	16 4	US-09-415-785A-85
31	13	0.6	16 4	US-08-944-465-85
32	13	0.6	16 4	US-09-415-868-85
33	13	0.6	16 4	US-09-415-868-85
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C 37	13	0.6	17 2	US-08-752-495-20
C 38	13	0.6	17 3	US-08-985-162-504
C 39	13	0.6	17 4	US-08-584-040-6041
C 40	13	0.6	17 4	US-09-450-195A-2
C 41	13	0.6	17 4	US-09-371-772B-2878
42	13	0.6	18 2	US-08-467-603-85
43	13	0.6	18 2	US-08-627-254C-14
44	13	0.6	18 2	US-08-466-793-85
45	13	0.6	18 2	US-08-491-861A-85

ALIGNMENTS

RESULT 1

US-09-198-452A-1839/c
; Sequence 1839, Application US/09198452A
; Patent No. 6559294

GENERAL INFORMATION:
; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198.452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 1839

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-1839

Query Match

Best Local Similarity 0.7%; Score 15; DB 4; Length 20;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 629 TATCCGAGCCGAG 643

Db 15 TATCCGAGCCGAG 1

RESULT 2

US-08-487-135B-10

; Sequence 10, Application US/08487135B

; Patent No. 5821122

GENERAL INFORMATION:

; APPLICANT: Yannick Guilleux; Francine Jotereau;
; APPLICANT: Thierry BoonFalleur; Sophie Lucas;
; APPLICANT: Vincent Brichard

; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES PERTIDES

; TITLE OF INVENTION: WHICH FORM COMPLEXES WITH MHC MOLECULE HLA-A2

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESS: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

COMPUTER: IBM PS/2

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 9, 2003, 04:11:53 ; Search time 105 Seconds
(without alignments)
8508.185 Million cell updates/sec

Title: US-09-856-327-1_COPY_1_2024
Perfect score: 2024
Sequence: 1 atcagcagctctctctca.....ttatggcactatgattcatg 2024

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 500186

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/6C COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	0.7	20	4	US-09-198-452A-1839
C 2	15	0.7	22	1	US-08-487-135B-10
C 3	15	0.7	22	2	US-08-915-972A-10
C 4	15	0.7	22	2	US-09-177-909-10
C 5	15	0.7	24	2	US-08-553-304-2
C 6	15	0.7	27	2	US-08-639-857-27
C 7	14	0.7	17	1	US-08-374-155A-23
C 8	14	0.7	17	2	US-08-785-196-23
C 9	14	0.7	17	4	US-08-584-040-6039
C 10	14	0.7	17	4	US-08-584-040-6040
C 11	14	0.7	17	4	US-09-371-772B-2876
C 12	14	0.7	17	4	US-09-371-772B-2877
C 13	14	0.7	20	2	US-09-044-506A-13
C 14	14	0.7	20	3	US-08-850-347-12
C 15	14	0.7	20	3	US-08-990-065-12
C 16	14	0.7	20	3	US-09-379-523-2
C 17	14	0.7	20	4	US-09-600-770A-29
C 18	14	0.7	20	4	US-09-422-978-8208
C 19	14	0.7	20	4	US-09-198-452A-5504
C 20	14	0.7	22	4	US-09-193-612B-21
C 21	14	0.7	23	4	US-09-328-571A-6
C 22	14	0.7	24	4	US-09-146-580-17
C 23	14	0.7	24	4	US-09-638-544-12
C 24	14	0.7	25	1	US-08-753-147-119
C 25	14	0.7	27	2	US-08-922-171-6
C 26	14	0.7	27	4	US-09-242-913B-6
C 27	13	0.6	15	4	US-09-346-551-4

Sequence 4, Appli
Sequence 85, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 504, App
Sequence 6041, Ap
Sequence 2, Appli
Sequence 2878, Ap
Sequence 85, Appl
Sequence 14, Appl
Sequence 85, Appl
Sequence 85, Appl

US-10-001-344-4
US-09-415-784-85
US-09-415-785A-85
US-08-944-465-85
US-09-415-868-85
US-09-415-900-85
US-08-292-081A-19
US-08-292-081A-20
US-08-752-495-19
US-08-752-495-20
US-08-985-162-504
US-08-584-040-6041
US-09-450-195A-2
US-09-371-772B-2878
US-08-467-603-85
US-08-627-254C-14
US-08-466-793-85
US-08-491-861A-85

ALIGNMENTS

RESULT 1
US-09-198-452A-1839/C
; Sequence 1839, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:

; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1839
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1839

Query Match 0.7%; Score 15; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 629 TATTCGAGGCGGAG 643
DB 15 TATTCGAGGCGGAG 1

RESULT 2
US-08-487-135B-10
; Sequence 10, Application US/08487135B
; Patent No. 5821122
; GENERAL INFORMATION:

; APPLICANT: Yamick Guilloux; Francine Jotereau;
; APPLICANT: Thierry Bqob-Falleur; Sophie Lucas;
; APPLICANT: Vincent Brimhard
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES PEPTIDES
; TITLE OF INVENTION: WHICH FORM COMPLEXES WITH MHC MOLECULE HLA-A2
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,135B
FILING DATE: 07-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,135
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 582112man D
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5388
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-135B-10

Query Match 0.7%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 238 CGAAGAAGGAAGTGC 252
Db 8 CGAAGAAGGAAGTGC 22

RESULT 3
US-08-915-972A-10
Sequence 10, Application US/08915972A
Patent No. 5896145
GENERAL INFORMATION:
APPLICANT: Yannick Guilloux; Francine Jotereau;
APPLICANT: Thierry Boon-Falleur; Sophie Lucas;
APPLICANT: Vincent Brichard
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: COMPLEXES WITH MHC MOLECULE HLA-A2 AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,972A
FILING DATE: August 21, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,135
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5896145man D
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5388 - JEL/NDH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-915-972A-10

Query Match 0.7%; Score 15; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 CGAAGAAGGAAGTGC 252
Db 8 CGAAGAAGGAAGTGC 22

RESULT 4
US-09-177-909-10
Sequence 10, Application US/09177909
Patent No. 5958711
GENERAL INFORMATION:
APPLICANT: Yannick Guilloux; Francine Jotereau;
APPLICANT: Thierry Boon-Falleur; Sophie Lucas;
APPLICANT: Vincent Brichard
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES PEPTIDES WHICH
TITLE OF INVENTION: FORM COMPLEXES WITH MHC MOLECULE HLA-A2 AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,909
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/915,972
FILING DATE: August 21, 1997
APPLICATION NUMBER: 08/487,135
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5958711man D
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5388 - JEL/NDH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-177-909-10

Query Match 0.7%; Score 15; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 CGAAGAAGGAAGTGC 252
Db 8 CGAAGAAGGAAGTGC 22

RESULT 5
US-08-553-304-2/c
Sequence 2, Application US/08553304

Patent No. 5922549
GENERAL INFORMATION:
APPLICANT: Czernilofsky, Armin P.
APPLICANT: Weyer, Ulrike
APPLICANT: Young, Ian G.
TITLE OF INVENTION: Process for Screening Substances Having
TITLE OF INVENTION: a Modulating Effect on an Interleukin-5 Receptor Mediated
TITLE OF INVENTION: Cellular Signal Transduction Pathway
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: 20005
ZIP: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553.304
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP94/01735
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1480000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: NO
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..24
US-08-553-304-2

Query Match 0.7%; Score 15; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 GATGGCATTGCGCA 1146
DB 16 GATGGCATTGCGCA 2

RESULT 6
US-08-639-857-27
Sequence 27, Application US/08639857
Patent No. 5955318
GENERAL INFORMATION:
APPLICANT: Simons, J. N.
APPLICANT: Desai, S. M.
APPLICANT: Mushahwar, I. K.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR CONTROLLING THE
TITLE OF INVENTION: TRANSLATION OF HEPATITIS GB PROTEINS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd
CITY: Abbott Park
STATE: IL

Patent No. 5922549
GENERAL INFORMATION:
APPLICANT: Czernilofsky, Armin P.
APPLICANT: Weyer, Ulrike
APPLICANT: Young, Ian G.
TITLE OF INVENTION: Process for Screening Substances Having
TITLE OF INVENTION: a Modulating Effect on an Interleukin-5 Receptor Mediated
TITLE OF INVENTION: Cellular Signal Transduction Pathway
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: 20005
ZIP: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553.304
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP94/01735
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1480000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: NO
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..24
US-08-553-304-2

Query Match 0.7%; Score 15; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 GATGGCATTGCGCA 1146
DB 16 GATGGCATTGCGCA 2

RESULT 6
US-08-639-857-27
Sequence 27, Application US/08639857
Patent No. 5955318
GENERAL INFORMATION:
APPLICANT: Simons, J. N.
APPLICANT: Desai, S. M.
APPLICANT: Mushahwar, I. K.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR CONTROLLING THE
TITLE OF INVENTION: TRANSLATION OF HEPATITIS GB PROTEINS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd
CITY: Abbott Park
STATE: IL

COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639.857
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5793.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-0378
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-639-857-27

Query Match 0.7%; Score 15; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 GGACTGCCATGGTGG 1210
DB 1 GGACTGCCATGGTGG 15

RESULT 7
US-08-374-155A-23
Sequence 23, Application US/08374155A
Patent No. 5786140
GENERAL INFORMATION:
APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Schiweck, Hubert
APPLICANT: Kunz, Markwart
APPLICANT: Munir, Mohammed
TITLE OF INVENTION: Preparation of Acarlogenic Sugar
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garret &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374.155A
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05638.0006-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-374-155A-23

Query Match 0.7%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1205 TGGTGAAGAAGC 1218
|||||

Db 1 TGGTGAAGAAGC 14

RESULT 8
US-08-785-396-23
Sequence 23, Application US/08785396
Patent No. 5985622

GENERAL INFORMATION:
APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Schiweck, Hubert
APPLICANT: Kunz, Markwart
APPLICANT: Munir, Mohammed
TITLE OF INVENTION: Preparation of Acarigenic Sugar
TITLE OF INVENTION: Substitutes
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,396
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/374,155
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05638.0006-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-785-396-23

Query Match 0.7%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1205 TGGTGAAGAAGC 1218
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Db 1 TGGTGAAGAAGC 14

RESULT 9
US-08-584-040-6039/c
Sequence 6039, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6039:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-6039

Query Match 0.7%; Score 14; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1862 TGAGGAAGGAGCA 1875
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Db 17 TGAGGAAGGAGCA 4

RESULT 10
US-08-584-040-6040/c
Sequence 6040, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime

;/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
;/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
;/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
;/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
;/ TITLE OF INVENTION: GROWTH FACTOR
;/ NUMBER OF SEQUENCES: 8502
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Lyon & Lyon
;/ STREET: 633 West Fifth Street
;/ STREET: Suite 4700
;/ CITY: Los Angeles
;/ STATE: California
;/ COUNTRY: U.S.A.
;/ ZIP: 90071-2086
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;/ MEDIUM TYPE: storage
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: IBM P.C. DOS 5.0
;/ SOFTWARE: Word Perfect 5.1
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/584,040
;/ FILING DATE: January 11, 1996
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 60/005,974
;/ FILING DATE: October 26, 1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Warburg, Richard J.
;/ REGISTRATION NUMBER: 32,327
;/ REFERENCE/DOCKET NUMBER: 218/064
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (213) 489-1600
;/ TELEFAX: (213) 955-0440
;/ TELEX: 67-3510
;/ INFORMATION FOR SEQ ID NO: 6040:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 17 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ US-08-584-040-6040

Query Match 0.7%; Score 14; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1862 TGAGGAAGGAGCAA 1875
Db 14 TGAGGAAGGAGCAA 1

RESULT 11
US-09-371-772B-2876/c
;/ Sequence 2876, Application US/09371772B
;/ Patent No. 6566127
;/ GENERAL INFORMATION:
;/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
;/ APPLICANT: Pavco, Pam
;/ APPLICANT: McSwiggen, Jim
;/ APPLICANT: Stinchcomb, Dan
;/ APPLICANT: Escobedo, Jaime
;/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;/ FILE REFERENCE: MEHB00,876-J (237/198)
;/ CURRENT APPLICATION NUMBER: US/09/371,772B
;/ CURRENT FILING DATE: 1999-08-10
;/ PRIOR APPLICATION NUMBER: US 60/005,974
;/ PRIOR FILING DATE: 1995-10-26
;/ PRIOR APPLICATION NUMBER: US 08/584,040
;/ PRIOR FILING DATE: 1996-01-08
;/ NUMBER OF SEQ ID NOS: 14225
;/ SOFTWARE: Patentin version 3.0

;/ SEQ ID NO 2876
;/ LENGTH: 17
;/ TYPE: RNA
;/ ORGANISM: Mus sp.
;/ US-09-371-772B-2876

Query Match 0.7%; Score 14; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1862 TGAGGAAGGAGCAA 1875
Db 17 TGAGGAAGGAGCAA 4

RESULT 12

US-09-371-772B-2877/c
;/ Sequence 2877, Application US/09371772B
;/ Patent No. 6566127
;/ GENERAL INFORMATION:
;/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
;/ APPLICANT: Pavco, Pam
;/ APPLICANT: McSwiggen, Jim
;/ APPLICANT: Stinchcomb, Dan
;/ APPLICANT: Escobedo, Jaime
;/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
;/ FILE REFERENCE: MEHB00,876-J (237/198)
;/ CURRENT APPLICATION NUMBER: US/09/371,772B
;/ CURRENT FILING DATE: 1999-08-10
;/ PRIOR APPLICATION NUMBER: US 60/005,974
;/ PRIOR FILING DATE: 1995-10-26
;/ PRIOR APPLICATION NUMBER: US 08/584,040
;/ PRIOR FILING DATE: 1996-01-08
;/ NUMBER OF SEQ ID NOS: 14225
;/ SOFTWARE: Patentin version 3.0
;/ SEQ ID NO 2877
;/ LENGTH: 17
;/ TYPE: RNA
;/ ORGANISM: Mus sp.
;/ US-09-371-772B-2877

Query Match 0.7%; Score 14; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1862 TGAGGAAGGAGCAA 1875
Db 14 TGAGGAAGGAGCAA 1

RESULT 13
US-09-044-506A-13
;/ Sequence 13, Application US/09044506A
;/ Patent No. 5955443
;/ GENERAL INFORMATION:
;/ APPLICANT: Frank Bennett, Thomas Condon,
;/ APPLICANT: Shin Flournoy, Hong Zhang
;/ TITLE OF INVENTION: Antisense Modulation of PECAM-1
;/ NUMBER OF SEQUENCES: 68
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Jane Massey Licata, Esq.
;/ STREET: 66 E. Main Street
;/ CITY: Marlton
;/ STATE: NJ
;/ COUNTRY: USA
;/ ZIP: 08053
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;/ COMPUTER: IBM 486
;/ OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
;/ SOFTWARE: WORDPERFECT 5.1
;/ CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/044,506A
;; FILING DATE: March 19, 1998
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jane Massey Licata
;; REGISTRATION NUMBER: 32,257
;; REFERENCE/DOCKET NUMBER: ISPH-0271
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (609) 779-2400
;; TELEFAX: (609) 810-1454
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; ANTI-SENSE: Yes
US-09-044-506A-13

Query Match 0.7%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 ATCAAGGGAGCCTT 342
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DB 3 ATCAAGGGAGCCTT 16

RESULT 14
US-08-850-347-12/c
;; Sequence 12, Application US/08850347
;; Patent No. 6110742
;; GENERAL INFORMATION:
;; APPLICANT: Soreq, Hermona
;; APPLICANT: Seidman, Shlomo
;; APPLICANT: Eckstein, Fritz
;; TITLE OF INVENTION: SYNTHETIC ANTISENSE
;; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND PHARMACEUTICAL COMPOSITIONS
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Kohn & Associates
;; STREET: 30500 No. 6110742thwestern Hwy.
;; CITY: Farmington Hills
;; STATE: Michigan
;; COUNTRY: US
;; ZIP: 48334
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/850,347
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kohn, Kenneth I.
;; REGISTRATION NUMBER: 30,955
;; REFERENCE/DOCKET NUMBER: 2391.00057
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (248) 539-5050
;; TELEFAX: (248) 539-5055
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; ANTI-SENSE: YES

;; ORIGINAL SOURCE:
;; ORGANISM: mouse
US-08-850-347-12

Query Match 0.7%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 ATGAAATCGAGTTC 298
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DB 16 ATGAAATCGAGTTC 3

RESULT 15
US-08-990-065-12/c
;; Sequence 12, Application US/08990065
;; Patent No. 6121046
;; GENERAL INFORMATION:
;; APPLICANT: Soreq, Hermona
;; APPLICANT: Seidman, Shlomo
;; APPLICANT: Eckstein, Fritz
;; APPLICANT: Friedman, Alon
;; APPLICANT: Kaufman, Daniela
;; TITLE OF INVENTION: SYNTHETIC ANTISENSE
;; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND PHARMACEUTICAL COMPOSITIONS
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Kohn & Associates
;; STREET: 30500 No. 6121046thwestern Hwy. Suite 410
;; CITY: Farmington Hills
;; STATE: Michigan
;; COUNTRY: U.S.
;; ZIP: 48334
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/990,065
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/850,347
;; FILING DATE: 02-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,826
;; FILING DATE: 01-JAN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Montgomery, Ilene N.
;; REGISTRATION NUMBER: 38,972
;; REFERENCE/DOCKET NUMBER: 2391.00086
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (248) 539-5050
;; TELEFAX: (248) 539-5055
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; HYPOTHETICAL: NO
;; ANTI-SENSE: YES
US-08-990-065-12

Query Match 0.7%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 285 ATGAAATCGAGTTC 298
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Mon Nov 10 16:38:20 2003

us-09-856-327-1_copy_1_2024.011.rn1

Page 7

Db 16 ATGAAATCGAGTTC 3

Search completed: November 9, 2003, 04:37:31
Job time : 107 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 9, 2003, 04:15:58 ; Search time 4979 Seconds
(without alignments)
16630.063 Million cell updates/sec
Title: US-09-856-327-1_COPY_1_2024
Perfect score: 2024
Sequence: 1 atcagccatgtctctctcaaa.....ttatggcactatgattctatg 2024

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 915674

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.ov.*
- 5: gb.pat.*
- 6: gb.ph.*
- 7: gb.pl.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.sv.*
- 12: gb.un.*
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- 14: gb.ba.*
- 15: em.fun.*
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- 31: em.htg.inv.*
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- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	0.7	20	6 AR311302	AR311302 Sequence
C 2	15	0.7	21	6 E28761	E28761 Antitumor d
C 3	15	0.7	22	6 AR048539	AR048539 Sequence
C 4	15	0.7	22	6 AR075928	AR075928 Sequence
C 5	15	0.7	24	6 A41635	A41635 Sequence 2
C 6	15	0.7	25	6 AX116800	AX116800 Sequence
C 7	15	0.7	27	6 AR075137	AR075137 Sequence
C 8	14	0.7	17	6 AR086841	AR086841 Sequence
C 9	14	0.7	17	6 AR190551	AR190551 Sequence
C 10	14	0.7	17	6 AR190552	AR190552 Sequence
C 11	14	0.7	17	6 AX674681	AX674681 Sequence
C 12	14	0.7	17	6 AX728728	AX728728 Sequence
C 13	14	0.7	17	6 AX736906	AX736906 Sequence
C 14	14	0.7	19	6 AX686090	AX686090 Sequence
C 15	14	0.7	20	6 AR108199	AR108199 Sequence
C 16	14	0.7	20	6 AR166374	AR166374 Sequence
C 17	14	0.7	20	6 AR258058	AR258058 Sequence
C 18	14	0.7	20	6 AR296473	AR296473 Sequence
C 19	14	0.7	20	6 AR314967	AR314967 Sequence
C 20	14	0.7	20	6 AX019847	AX019847 Sequence
C 21	14	0.7	20	6 AX147403	AX147403 Sequence
C 22	14	0.7	20	6 AX601113	AX601113 Sequence
C 23	14	0.7	20	6 BD069712	BD069712 Synthetic
C 24	14	0.7	20	6 BD128502	BD128502 EF-Tu mRNA
C 25	14	0.7	20	6 BD136434	BD136434 Antisense
C 26	14	0.7	21	6 AX697037	AX697037 Sequence
C 27	14	0.7	22	6 AR287188	AR287188 Sequence
C 28	14	0.7	23	6 AX703118	AX703118 Sequence
C 29	14	0.7	23	6 A61993	A61993 Sequence 23
C 30	14	0.7	23	6 AR217287	AR217287 Sequence
C 31	14	0.7	23	6 BD063910	BD063910 Nucleic a
C 32	14	0.7	24	6 AR174339	AR174339 Sequence
C 33	14	0.7	24	6 AR309102	AR309102 Sequence
C 34	14	0.7	24	6 AX138601	AX138601 Sequence
C 35	14	0.7	24	6 AX193737	AX193737 Sequence
C 36	14	0.7	24	6 AX292697	AX292697 Sequence
C 37	14	0.7	24	6 BD137081	BD137081 Human che
C 38	14	0.7	25	6 AX190653	AX190653 Sequence
C 39	14	0.7	25	6 BD141017	BD141017 Transgeni
C 40	14	0.7	25	6 BD167283	BD167283 Gene enco
C 41	14	0.7	25	6 BD170016	BD170016 Aip-1/FLA
C 42	14	0.7	27	6 A43124	A43124 Sequence 10
C 43	14	0.7	27	6 AR088552	AR088552 Sequence
C 44	14	0.7	27	6 AR307600	AR307600 Sequence
C 45	14	0.7	27	6 AX260322	AX260322 Sequence

ALIGNMENTS

RESULT 1
AR311302/c
LOCUS AR311302 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1839 from patent US 6559294.
ACCESSION AR311302
VERSION AR311302.1 GI:31704728
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 1839 06-MAY-2003,

FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 5 a 5 c 6 g 4 t
ORIGIN

Query Match 0.7%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 629 TATTCGAGGCCGAG 643
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Db 15 TATTCGAGGCCGAG 1

RESULT 2
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LOCUS E28761
DEFINITION Antitumor drug.
ACCESSION E28761
VERSION E28761.1 GI:13018399
KEYWORDS JP 199225762-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kozo.N., Masami.M., Makiko.S., Hiroshi.K. and Yoshinori.F.
TITLE Antitumor drug
JOURNAL TORAY IND INC
COMMENT OS Unidentified
PN JP 199225762-A/3
PD 24-AUG-1999
PF 10-FEB-1998 JP 1998028922
PI Kozo Nagai, Masami MoriYama, Makiko Saito, Hiroshi Kogo, Pi Yoshinori Fujimoto
PC C12N15/09 A61K35/76 A61K48/00 A61K48/00 C12N5/10 PC C12P21/02/A61K38/00,
PC C12P21/02 C12R1.91, C12N15/00, C12N5/00 A61K37/02 CC
Topology: Linear;
FH Key Location/Qualifiers
FT source 1..21
/organism="Unidentified".
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source Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 4 a 5 c 6 g 6 t
ORIGIN

Query Match 0.7%; Score 15; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1668 CAGTGGCTGATAACA 1682
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Db 20 CAGTGGCTGATAACA 6

RESULT 3
AR048539
LOCUS AR048539
DEFINITION Sequence 10 from patent US 5821122.
ACCESSION AR048539
VERSION AR048539.1 GI:5970882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Guillaux, Y., Jotereau, F., Boon-Palleur, T., Lucas, S. and Brichard, V.

FEATURES
source Location/Qualifiers
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/organism="unknown"
BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN

Query Match 0.7%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 238 CGAAGAGGACTGC 252
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Db 8 CGAAGAGGACTGC 22

RESULT 4
AR075928
LOCUS AR075928
DEFINITION Sequence 10 from patent US 5958711.
ACCESSION AR075928
VERSION AR075928.1 GI:10002674
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Guillaux, Y., Jotereau, F., Boon-Palleur, T., Lucas, S. and Brichard, V.
TITLE Methods for determining expression of NAG tumor rejection antigen precursor
JOURNAL Patent: US 5958711-A 10 28-SEP-1999;
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source Location/Qualifiers
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BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN

Query Match 0.7%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 238 CGAAGAGGACTGC 252
|||||
Db 8 CGAAGAGGACTGC 22

RESULT 5
A41635/c
LOCUS A41635
DEFINITION Sequence 2 from Patent WO9428170.
ACCESSION A41635
VERSION A41635.1 GI:2297268
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Czernilofsky, A.P., Weyer, U. and Young, I.G.
TITLE PROCESS FOR SCREENING SUBSTANCES HAVING A MODULATING EFFECT ON AN INTERLEUKINE-5-RECEPTOR-DEPENDENT CELLULAR SIGNAL TRANSMISSION PATH
JOURNAL Patent: WO 9428170-A 2 08-DEC-1994;
COMMENT BOEHRINGER INGELHEIM INT (DE)
Other publication AU 6997794 941220
Other publication NO 954781 960123
Other publication FI 955700 951127
Other publication DE 4317577 941201.
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source Location/Qualifiers
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/db_xref="taxon:32644"

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BASE COUNT 10 a 1. .24 5 c 5 g 4 t
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Query Match
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 GATGGCATTTCGCCA 1146
Db 16 GATGGCATTTCGCCA 2

RESULT 6
AX116800
LOCUS AX116800 25 bp DNA PAT 11-MAY-2001
DEFINITION Sequence 1923 from Patent WO0129262.
ACCESSION AX116800
VERSION AX116800.1 GI:14033742
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1923 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 3 a 6 c 8 g 8 t
ORIGIN

Query Match
Best Local Similarity 0.7%; Score 15; DB 6; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 CTTGTCTGCGGAGGC 483
Db 11 CTTGTCTGCGGAGGC 25

RESULT 7
AR075137
LOCUS AR075137 27 bp DNA PAT 28-AUG-2000
DEFINITION Sequence 27 from patent US 5955318.
ACCESSION AR075137
VERSION AR075137.1 GI:10001889
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Simons,J.N., Desai,S.M. and Mushahwar,I.K.
TITLE Reagents and methods useful for controlling the translation of hepatitis B proteins
JOURNAL Patent: US 5955318-A 27 21-SEP-1999;
FEATURES
source
1. .27
/organism="unknown"

BASE COUNT 9 a 3 c 10 g 5 t
ORIGIN

Query Match
Best Local Similarity 0.7%; Score 15; DB 6; Length 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 GGACTGCCATGTGG 1210
|||||

Db 1 GGACTGCCATGTGG 15

RESULT 8
AR086841
LOCUS AR086841 17 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 23 from patent US 5985622.
ACCESSION AR086841
VERSION AR086841.1 GI:10013607
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Mattes,R., Klein,K., Schiweck,H., Kunz,M. and Munir,M.
TITLE Preparation of acarogenic sugar substitutes
JOURNAL Patent: US 5985622-A 23 15-NOV-1999;
FEATURES
source
1. .17
/organism="unknown"

BASE COUNT 5 a 1 c 7 g 4 t
ORIGIN

Query Match
Best Local Similarity 0.7%; Score 14; DB 6; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1205 TGGTGGAGAGGC 1218
Db 1 TGGTGGAGAGGC 14

RESULT 9
AR190551/c
LOCUS AR190551 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 6039 from patent US 6346398.
ACCESSION AR190551
VERSION AR190551.1 GI:20236516
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6039 12-FEB-2002;
FEATURES
source
1. .17
/organism="unknown"

BASE COUNT 2 a 7 c 2 g 6 t
ORIGIN

Query Match
Best Local Similarity 0.7%; Score 14; DB 6; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1862 TGAGGAGGAGCAA 1875
Db 17 TGAGGAGGAGCAA 4

RESULT 10
AR190552/c
LOCUS AR190552 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 6040 from patent US 6346398.
ACCESSION AR190552
VERSION AR190552.1 GI:20236517
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6040 12-FEB-2002;
FEATURES Location/Qualifiers
1. .17
/organism="unknown"
BASE COUNT 1 a 7 c 1 g 8 t
ORIGIN

Query Match 0.7%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1862 TGAGGAGGAGCA 1875
Db 14 TGAGGAGGAGCA 1

RESULT 11
AX674681/c
LOCUS AX674681 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 3126 from Patent WO03004526.
ACCESSION AX674681
VERSION AX674681.1 GI:29333029
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
JOURNAL Patent: WO 03004526-A 3126 16-JAN-2003;
FEATURES Molecular Engines Laboratories (FR)
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 2 c 4 g 6 t
ORIGIN

Query Match 0.7%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1298 CCATTACAGAGA 1311
Db 16 CCATTACAGAGA 3

RESULT 12
AX728728/c
LOCUS AX728728 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 362 from Patent WO03025175.
ACCESSION AX728728
VERSION AX728728.1 GI:30508071
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 362 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
Location/Qualifiers

source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 6 c 4 g 5 t
ORIGIN

Query Match 0.7%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 CGTGAGCAGCA 1532
Db 16 CGTGAGCAGCA 3

RESULT 13
AX736906/c
LOCUS AX736906 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2496 from Patent WO03025177.
ACCESSION AX736906
VERSION AX736906.1 GI:30516194
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL Patent: WO 03025177-A 2496 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 2 c 4 g 6 t
ORIGIN

Query Match 0.7%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1298 CCATTACAGAGA 1311
Db 16 CCATTACAGAGA 3

RESULT 14
AX686090
LOCUS AX686090 19 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 134 from Patent WO02064791.
ACCESSION AX686090
VERSION AX686090.1 GI:29371908
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences

REFERENCE 1
AUTHORS Alsobrook II, J. P., Anderson, D. W., Burgess, C. E., Boldog, F. L., Casman, S. J., Colman, S. D., Edinger, S. R., Ellerman, K., Garlach, V., Gorman, L., Grosse, W. M., Guo, X., Herrmann, J. L., Kekuda, R., Lepley, D. M., Li, L., MacDougall, J. R., Millet, I., Pena, C. E., Peyman, J. A., Rastelli, L., Rieger, D. K., Shimkets, R. A., Smithson, G., Spytek, K. A., Stone, D. J., Tchernev, V. T., Vernet, C. A., Voss, E. Z., Zerbuzen, B. D., Zhong, H. and Zhong, M.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 02064791-A 134 22-AUG-2002;
FEATURES Curegen Corporation (US)
Location/Qualifiers

source 1. .19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="oligonucleotide primer"
BASE COUNT 5 a 8 c 3 g 3 t
ORIGIN

Query Match 0.7%; Score 14; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1309 AGAACACCCCTGGC 1322
* |||||/|||||
Db 1 AGAACACCCCTGGC 14

RESULT 15
ARI08199/c
LOCUS ARI08199 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 12 from patent US 6110742.
ACCESSION ARI08199
VERSION ARI08199.1 GI:12823686
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Soreq, H., Seidman, S. and Eckstein, P.
TITLE Synthetic antisense oligodeoxynucleotides targeted to AChE
JOURNAL Patent: US 6110742-A 12-29-AUG-2000;
FEATURES
source Location/Qualifiers
1. .20
/organism="unknown"

BASE COUNT 6 a 5 c 3 g 6 t
ORIGIN

Query Match 0.7%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 285 ATGAATCGAGTTC 298
* |||||/|||||
Db 16 ATGAATCGAGTTC 3

Search completed: November 9, 2003, 06:00:52
Job time : 4982 secs

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OM nucleic - nucleic search, using sw model

Run on: November 9, 2003, 03:24:12 / Search time 401 seconds
(without alignments)
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Perfect score: 2024
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Scoring table: OLIGO.NUC
Gapop 60.0, Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

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Minimum DB seq length: 15

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25: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2004.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	0.7	20	AA92538	PCR primer used to
C 2	15	0.7	21	AA210152	PR-39 peptide PCR
C 3	15	0.7	22	AA761263	NAG tumour rejecti
C 4	15	0.7	24	AA800001	Murine IL-5 recept
C 5	15	0.7	25	AA257422	Oligonucleotide PC
C 6	15	0.7	25	AAH39127	SNP specific SNPE
C 7	15	0.7	27	AA759804	Hepatitis GB virus
C 8	14	0.7	17	AA73289	Mouse flk-1 VEGF r

C 9	14	0.7	17	18	AA73290	Mouse flk-1 VEGF r
C 10	14	0.7	17	18	AA76193	Human IL4 receptor
C 11	14	0.7	17	20	AA53990	Human IL-4 receptor
C 12	14	0.7	17	21	AA19556	Human IL4 receptor
C 13	14	0.7	17	21	AA33434	Low adenosine anti
C 14	14	0.7	17	25	ABT34725	Tumour suppression
C 15	14	0.7	19	24	AB564426	Human NOVX forward
C 16	14	0.7	19	25	AA54402	rpOB gene oligomer
C 17	14	0.7	19	25	AAV41291	Antisense oligo ma
C 18	14	0.7	20	19	AAZ08891	Human PECAM-1 anti
C 19	14	0.7	20	20	AAZ99766	EF-Tu gene region
C 20	14	0.7	20	20	AAZ96178	PCR primer used to
C 21	14	0.7	20	20	AAZ56439	Mouse flk-1 PCR fo
C 22	14	0.7	20	20	AAZ73852	Human biallelic ma
C 23	14	0.7	20	22	AAH47747	C. histolyticum cl
C 24	14	0.7	20	22	AAH44822	Antisense oligonuc
C 25	14	0.7	20	25	ABZ68895	RT-PCR primer used
C 26	14	0.7	20	25	ABT21477	Multiplex group PC
C 27	14	0.7	20	25	AAZ37188	Human PRO1315 forw
C 28	14	0.7	21	22	AAZ54275	Primer #26 used in
C 29	14	0.7	22	20	AAZ77004	PCR primer PHN2197
C 30	14	0.7	22	24	ABZ58999	Human G-protein co
C 31	14	0.7	22	24	ABT04366	Human G-protein co
C 32	14	0.7	23	18	AAZ25346	Primer for H.pylori
C 33	14	0.7	23	18	AAZ46890	3' primer amplifie
C 34	14	0.7	23	18	AAZ60471	MCSP PCR primer RM
C 35	14	0.7	23	18	AAZ77528	3' primer for H. p
C 36	14	0.7	23	19	AAZ30505	Oligonucleotide pr
C 37	14	0.7	23	19	AAZ30664	Oligonucleotide pr
C 38	14	0.7	23	20	AAZ58859	H. pylori OMP DNA
C 39	14	0.7	23	20	AAZ03615	Rio Mamore Hantavi
C 40	14	0.7	23	24	ABQ78803	PCR primer used to
C 41	14	0.7	24	20	AAZ89400	Human MACK gene OR
C 42	14	0.7	24	20	AAZ73827	Mutagenic primer #
C 43	14	0.7	24	22	AAZ84286	Human GM-CSF rever
C 44	14	0.7	24	24	ABU40466	Human MEC cDNA amp
C 45	14	0.7	24	24	AB191314	Capture oligonucle

ALIGNMENTS

RESULT 1
AA92538/c
ID AA92538 standard; DNA; 20 BP.

AC AA92538;

XX AA92538;

DT 13-SEP-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.

DE Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; PCR primer; ss.

OS Synthetic.

OS Chlamydia pneumoniae.

PN WO9927105-A2

XX 03-JUN-1999.

XX 20-NOV-1998; 98MO-IE01890.

XX 04-NOV-1998; 98US-0107078.

XX 21-NOV-1997; 97FR-0014673.

PA (GEST) GENSET.

XX Griffiths R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae
PT Page 1519; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading
CC frames and other nucleic acid sequences from the genome of
CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC disease such as pneumonia and bronchitis and is thought to be a
CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC containing C. pneumoniae nucleotide sequences can also be used as
CC immunogenic compositions, especially where the vector directs the
CC expression of a neutralising epitope of C. pneumoniae.
XX
XX Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 other;
SQ

Query Match 0.7%; Score 15; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 629 TATTCGAGGCCGAG 643
DB 15 TATTCGAGGCCGAG 1

RESULT 2
AAZ10152/c
ID AAZ10152 standard; DNA; 21 BP.
XX
XX AAZ10152;
AC
XX
XX 05-NOV-1999 (first entry)
DT
DE PR-39 peptide PCR primer SEQ ID NO:3.
XX
XX Antitumour; antimicrobial; cathelin; defensin; PR-39; inhibition;
KW tumour metastasis; swine skin lesion; PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX JF11225762-A.
FN
XX
XX 24-AUG-1999.
PD
XX
XX 10-FEB-1998; 98JP-0028922.
PP
XX 10-FEB-1998; 98JP-0028922.
PR
XX (TORA) TORAY IND INC.
PA
XX WPI; 1999-521078/44.
DR
XX Antimicrobial peptide gene - useful as antitumour agent
PT
XX
XX Claim 12; Page 11; 12pp; Japanese.
PS
XX
XX An antitumour agent has been developed comprising an antimicrobial
CC peptide gene, particularly a cathelin or defensin family peptide gene,
CC especially the PR-39 peptide gene derived from polynuclear leukocyte
CC in swine skin lesion or small intestine. Also described in the present
CC invention is an antitumour agent composed of an effective ingredient of
CC a vector, particularly pRC/CMV expression vector, with the antimicrobial
CC peptide gene integrated. Transduction of an antimicrobial peptide gene
CC in tumour cells inhibits the infiltration activity of tumour cells,
CC induces morphological changes of cells, decomposes actin-filament
CC structure and leads to the inhibition of tumour metastasis. The present
CC sequence represents a specifically claimed PCR primer for PR-39.
XX
XX Sequence 21 BP; 4 A; 5 C; 6 G; 6 T; 0 other;
SQ

Query Match 0.7%; Score 15; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1668 CAGTGGCTGATAACA 1682
DB 20 CAGTGGCTGATAACA 6

RESULT 3
AAT61263
ID AAT61263 standard; DNA; 22 BP.
XX
XX AAT61263;
AC
XX 23-JUN-1997 (first entry)
DT
XX
XX NAG tumour rejection antigen probe.
DE
XX
XX NAG; tumour rejection antigen precursor; TRAP; HLA-A2; MHC;
KW major histocompatibility complex; cytolytic T lymphocyte; CTL;
KW melanoma; adoptive immunotherapy; vaccine; therapy; diagnosis;
KW N-acetylglucosaminyltransferase V; Gnt-V; probe; ss.
XX
XX Synthetic.
OS
XX
XX WO9640039-A2.
PN
XX
XX 19-DEC-1996.
PD
XX
XX 07-MAY-1996; 96WO-US06409.
PP
XX
XX 07-JUN-1995; 95US-0487135.
PR
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
XX Boon-Falleur T, Brichard V, Guilloux Y, Jotereau F;
PI Lucas S;
PI
XX
XX WPI; 1997-099872/09.
DR
XX
XX
XX New nucleic acid encoding the tumour rejection antigen precursor NAG
PT - and related protein, antigenic peptide(s), vectors and host cells,
PT useful for inducing cytolytic T cell response, esp. to melanoma
XX
XX Example 10; Page 12; 46pp; English.
PS
XX
XX DNA probe A (AAT61263) was used to examine SacI-digested fragments
CC of a 14 kb insert (see also AAT61272-73) that had been obtd. from a
CC genomic library of melanoma M22-MEL.2.2.5 using a probe based on
CC nucleotides 48-185 of clone 560E1 (see also AAT61258). Probe A
CC hybridised to a 5.5 kb fragment of the 14 kb insert. This
CC fragment was found to correspond to a exon A of
CC N-acetylglucosaminyltransferase V cDNA. An intronic region
CC following exon A includes a sequence coding for novel NAG tumour
CC rejection antigens (AAW11695-96).
XX
XX Sequence 22 BP; 6 A; 4 G; 7 G; 5 T; 0 other;
SQ

Query Match 0.7%; Score 15; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 238 CGAAGAGGAACTGC 252
DB 8 CGAAGAGGAACTGC 22

RESULT 4
AAQ80001/c
ID AAQ80001 standard; DNA; 24 BP.
XX

AC AAQ80001;
 XX 25-MAR-2003 (updated)
 DT 04-AUG-1995 (first entry)
 XX Murine IL-5 receptor alpha-subunit PCR primer MF73.
 DE Interleukin-5 receptor; mIL-5R; alpha-subunit;
 KW receptor-dependent signal transfer; regulation; modulation; ss.
 XX Synthetic.
 OS DE4317577-A1.
 XX 01-DEC-1994.
 XX 27-MAY-1993; 93DE-4317577.
 XX 27-MAY-1993; 93DE-4317577.
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX Czernilofsky AP, Weyer U, Young IG;
 XX WPI; 1995-007479/02.
 XX Detecting cpds. that modulate receptor dependent signal transfer
 PT - using cells contg. a reporter gene under control of regulators
 PT which respond to concn. change in messengers of an IL-5 receptor
 PT coupled pathway, also new transformed cells and DNA constructs.
 XX Example 2; Page 10; 18pp; German.
 XX Primers MF71 and MF73 (AAQ80000 and AAQ80001) amplified a 1272 bp PCR
 CC product comprising the murine IL-5 receptor coding region as part of
 CC a cloning procedure for expressing the IL-5 receptor in FDC-P1 cells.
 CC The transformed cells also contain a reporter gene and a regulatory
 CC sequence which responds to a change in concentration of 1 or more
 CC secondary messengers of the IL-5 receptor-coupled pathway;
 CC expression of the reporter gene is modulated by a concentration
 CC change of the messenger. The cells are then used to assay the
 CC modulating effect of a candidate substance on the IL-5 receptor
 CC dependent signal transfer pathway.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 24 BP; 10 A; 5 C; 5 G; 4 T; 0 other;
 SQ Query Match 0.7%; Score 15; DB 15; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1132 GATGGCATTGCGCA 1146
 DB ||||||||||||
 16 GATGGCATTGCGCA 2
 RESULT 5
 AA257422/c
 ID AA257422 standard; DNA; 25 BP.
 XX AAZ57422;
 AC AAZ57422;
 XX 07-APR-2000 (first entry)
 DT Oligonucleotide PCR primer pair #2 primer #2.
 DE PCR primer; Zaocys dhumnade; Tortoise plastron; Oviductus ranae;
 KW discrimination; black snake; forest frog; oil; reagent box;
 KW medicinal; ss.
 XX Synthetic.
 OS CN1232085-A.
 PN

XX 20-OCT-1999.
 PD 31-MAR-1999; 99CN-0114133.
 XX 31-MAR-1999; 99CN-0114133.
 PR (UYNA-) UNIV NANJING.
 PA Wang Y, Zhou K, Liu Z;
 XX WPI; 2000-098492/09.
 XX Polymerase chain reaction (PCR) determining primer for Zaocys dhumnade,
 PT Tortoise plastron and Oviductus ranae -
 PT Claim 1; Page 1; 4pp; Chinese.
 XX The present invention describes a special DNA sequence which can be used
 CC to synthesise three pairs of high-specificity primers useful for
 CC discriminating if black snake, tortoise plastron and forest frog oil are
 CC true or false by simple polymerase chain reaction (PCR) of their DNA.
 CC AAZ57419 to AAZ57424 represent specifically claimed primers from the
 CC present invention. The primers can be used to make a reagent box for
 CC discriminating medicinal materials with high speed and quality.
 XX Sequence 25 BP; 5 A; 8 C; 7 G; 5 T; 0 other;
 SQ Query Match 0.7%; Score 15; DB 21; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1361 GTCGGTCTCGAGTG 1375
 DB ||||||||||||
 18 GTCGGTCTCGAGTG 4
 RESULT 6
 AAH39127
 ID AAH39127 standard; DNA; 25 BP.
 XX AAH39127;
 AC AAH39127;
 XX 14-AUG-2001 (first entry)
 DT SNP specific SNPE primer SEQ ID 1923.
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 KW Leshch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; primer; ss.
 XX Homo sapiens.
 OS WO200129262-A2;
 XX 26-APR-2001;
 PD 13-OCT-2000; 2000WO-US28436.
 XX 15-OCT-1999; 99US-0160096.
 XX (ORCH-) ORCHID BIOSCIENCES INC.
 PA Picoult-Newburg L, Pohl M;
 XX WPI; 2001-290930/30.
 XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample -

CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.
XX

SQ Sequence 17 BP; 2 A; 7 C; 2 G; 6 U; 0 other;
Query Match 0.7%; Score 14; DB 18; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1862 TGAGGAGGAGCAA 1875

DB 17 TGAGGAGGAGCAA 4

RESULT 9

AAX73290/c
ID AAX73290 standard; RNA; 17 BP.

AC AAX73290;

DT 28-JUL-1999 (first entry)

DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #723.

KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.

OS Mus sp.

PN W09715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US17480.

PR 11-JAN-1996; 96US-0584040.

PR 26-OCT-1995; 95US-0005974.

XX (CHIR) CHIRON CORP.

PA (RIBO-) RIBOZYME PHARM INC.

XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient

PS Claim 4; Page 146; 218pp; English.

CC The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention.

XX Sequence 17 BP; 1 A; 7 C; 1 G; 8 U; 0 other;

Query Match 0.7%; Score 14; DB 18; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1862 TGAGGAGGAGCAA 1875

|||||

DB 14 TGAGGAGGAGCAA 1

RESULT 10

AAT76193/c

ID AAT76193 standard; DNA; 17 BP.

XX AC AAT76193;

XX 12-SEP-1997 (first entry)

XX Human IL4 receptor antisense oligonucleotide.

XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; interleukin; ss.

OS Synthetic.

XX W09640162-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US09306.

XX 07-JUN-1995; 95US-0474497.

XX (UYEC-) UNIV EAST CAROLINA.

XX Metzger WJ; Nyce JW;

XX WPI; 1997-051871/05.

XX Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligonucleotide to airway epithelium of
PT subject

XX Example 5; Page 29; 71pp; English.

CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC specific for the human IL4 receptor. The method can be used to
CC treat airway diseases such as cystic fibrosis, asthma, chronic
CC obstructive pulmonary disease, bronchitis and other airway diseases
CC characterised by an inflammatory response. By eliminating adenosine from
CC the antisense ON, its liberation upon antisense degradation is
CC prevented, thereby preventing adenosine-induced bronchoconstriction in
CC patients with hyper-reactive airways.

XX Sequence 17 BP; 0 A; 5 C; 5 G; 7 T; 0 other;

Query Match 0.7%; Score 14; DB 18; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.7e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 590 AACGACCCGCGAGA 603

|||||

DB 14 AACGACCCGCGAGA 1

RESULT 11

AAX53990/c

ID AAX53990 standard; DNA; 17 BP.

XX AC AAX53990;

XX 05-JUL-1999 (first entry)

XX Human IL-4 receptor antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;

pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; pain; cystic fibrosis;
pulmonary hypertensive; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
prostate cancer; ss.

XX
OS Synthetic.
PN WO9913886-A1.
PD 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US19419.
PF XX
PP XX
PR 09-JUN-1998; 98US-0093972.
PR 17-SEP-1997; 97US-0059160.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction
PS Disclosure; Page 49; 120pp; English.
XX

The specification describes antisense oligonucleotides (AAx52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAx5272-74. These multiple target oligonucleotides (specifically AAx55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.

XX
SQ Sequence 17 BP; 0 A; 5 C; 5 G; 7 T; 0 other;

Query Match 0.7%; Score 14; DB 20; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 590 AACGACCCGGCGA 603
|||||
DB 14 AACGACCCGGCGA 1

RESULT 12
AAF19556/c
ID ID AAF19556 standard; DNA; 17 BP.
XX
XX AAF19556;
DT 14-MAR-2001 (first entry)
XX
DE Human IL4 receptor polynucleotide fragment #1123.
XX

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; ADS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

Homo sapiens.

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US08020.

06-APR-1999; 99US-0127958.

(UYEC-) UNIV EAST CAROLINA.
(NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

Claim 14; Page 208; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy (fies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAP18434 to AAP21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

```

XX
SQ Sequence 17 BP, 0 A, 5 C, 5 G, 7 T, 0 other;
Query Match 0.7%; Score 14; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 590 AACGACCCGGCAGA 603
Db 14 AACGACCCGGCAGA 1

```

Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 590 AACGACCCGGCAGA 603
DB 14 AACGACCCGGCAGA 1

RESULT 14
ABT34725/C
ID ABT34725 standard; DNA; 17 BP.
XX
AC ABT34725;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 362.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB04208.
XX
PR 17-SEP-2001; 2001PR-0011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Anson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases
PT associated with tumors and cell degeneration, also related
PT polypeptides, antibodies and transfected cells -
XX
PS Disclosure; Page 76; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15
CC consecutive nucleotides from the 17 mer sequence, a sequence with, after
CC optimal alignment, at least 80 % identity to the 17 mer sequence, a
CC sequence that hybridizes to them under highly stringent conditions, or
CC the complement of any of them, or the corresponding RNA. The novel
CC isolated nucleic acids of the invention are useful as probes and primers
CC for detecting, identifying, quantifying and/or amplifying a nucleic acid,
CC e.g. as one component of a gene chip, in vitro as (anti)sense reagents,
CC and for production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention.

XX
SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 other;

Query Match
Best Local Similarity 0.7%; Score 14; DB 25; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
AAA33434/C
ID AAA33434 standard; DNA; 17 BP.
XX
AC AAA33434;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:1123.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Claim 18; Page 405; 1343pp; English.

XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.

XX
SQ Sequence 17 BP; 0 A; 5 C; 5 G; 7 T; 0 other;

Query Match
Best Local Similarity 0.7%; Score 14; DB 21; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 CGTGAGCAAGGA 1532
|||||
Db 16 CGTGAGCAAGGA 3

RESULT 15
ABS64426
ID ABS64426 standard; DNA; 19 BP.

XX AC ABS64426;
XX DT 15-NOV-2002 (first entry)
XX DE Human NOVX forward PCR primer Ag2493.

XX Human; NOVX; neurodegenerative disease; Alzheimer's disease; anxiety;
KW Parkinson's disease; Huntington's disease; neurological disorder;
KW schizophrenia; manic depression; mental retardation; angina pectoris;
KW cardiovascular disease; acute heart failure; myocardial infarction;
KW muscular disease; muscular disorder; retinal disease; photoreception;
KW deafness; keratinisation disorder; cancer; ovarian cancer; melanoma;
KW immunological disorder; inflammatory disease; immune disease; diabetes;
KW bacterial infection; fungal infection; protozoal infection; obesity;
KW viral infection; reproductive system disorder; metabolic disturbance;
KW anorexia; wasting disorder; chronic disease; infectious disease;
KW dyslipidaemia; PCR; primer; ss.

XX OS Homo sapiens.

XX PN WO200264791-A2.

XX PD 22-AUG-2002.

XX PF 10-DEC-2001; 2001WO-US48369.

XX PR 08-DEC-2000; 2000US-254329P.

XX PR 14-DEC-2000; 2000US-255648P.

XX PR 15-MAY-2001; 2001US-291037P.

XX PR 08-JUN-2001; 2001US-297173P.

XX PR 08-JUN-2001; 2001US-309258P.

XX PR 29-AUG-2001; 2001US-315639P.

XX PR 01-OCT-2001; 2001US-326393P.

XX PA (CURA-) CURAGEN CORP.

XX PI Alcobrook JP, Anderson DW, Burgess CE, Boldog FL, Casman SJ;
PI Colman SD, Edinger SR, Ellerman K, Gerlach V, Gorman L, Grosse WM;
PI Guo X, Herrmann JL, Kekuda R, Lepley DM, Li L, MacDougall JR;
PI Millett I, Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Tchernev VT, Vernet CAM, Voss EZ;
PI Zerhusen BD, Zhong H, Zhong M;

XX WPI; 2002-643486/69.

XX PT New NOVX polypeptides and polynucleotides useful for treating or
PT preventing e.g. neurodegenerative diseases, neurological disorders,
PT cardiovascular diseases, muscular diseases and disorders, or
PT immunological diseases

XX PS Example 2; Page 255; 299pp; English.

XX CC The present invention relates to new NOVX polypeptides. The polypeptides,
CC polynucleotides and antibodies are useful in the manufacture of a
CC medicament for treating or preventing neurodegenerative diseases (e.g.
CC Alzheimer's disease, Parkinson's disease, or Huntington's disease),
CC neurological disorders (e.g. anxiety, schizophrenia, manic depression or
CC mental retardation), cardiovascular disease (e.g. acute heart failure,
CC angina pectoris or myocardial infarction), muscular diseases and
CC disorders, retinal diseases (including those involving photoreception,
CC deafness and keratinisation disorders), cancer (e.g. ovarian cancer or
CC melanoma), immunological disorders, inflammatory and immune diseases,
CC bacterial, fungal, protozoal and viral infections, and reproductive

CC system disorders. The proteins of the invention may be used to screen
CC drugs or compounds that modulate the NOVX protein activity or expression,
CC as well as to treat disorders characterised by insufficient or excessive
CC production of NOVX protein or protein forms that have decreased or
CC aberrant activity compared to NOVX wild type protein, such as diabetes,
CC obesity, metabolic disturbances associated with obesity, anorexia and
CC wasting disorders associated with chronic diseases and various cancers,
CC infectious diseases and various dyslipidaemias. The nucleic acid
CC sequences of the invention may be used in chromosome mapping,
CC identifying an individual from minute biological samples (tissue typing),
CC and in forensic identification of a biological sample. The present
CC nucleic acid sequence represents a PCR primer that was used in the
CC methods of the invention for amplification of NOVX genes.

XX SQ Sequence 19 BP; 5 A; 8 C; 3 G; 3 T; 0 other;

Query Match 0.74; Score 14; DB 24; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1309 AGAACACCCCTGGC 1322

Db 1 AGAACACCCCTGGC 14

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	17	0.8	25	14	US-10-098-263B-111281
C 2	16	0.8	25	14	US-10-098-263B-53235
C 3	15	0.7	25	14	US-10-098-263B-22077
C 4	15	0.7	25	14	US-10-098-263B-39977
C 5	15	0.7	25	14	US-10-098-263B-41699
C 6	15	0.7	25	14	US-10-098-263B-64985
C 7	15	0.7	25	14	US-10-098-263B-101971
C 8	14	0.7	17	12	US-10-339-782-485
C 9	14	0.7	17	14	US-10-061-249-23
C 10	14	0.7	19	14	US-10-058-442-19
C 11	14	0.7	20	14	US-10-215-271-15
C 12	14	0.7	21	11	US-09-946-374-105
C 13	14	0.7	21	12	US-10-015-387A-105
C 14	14	0.7	21	12	US-10-227-596-5
C 15	14	0.7	21	12	US-10-006-130A-105
C 16	14	0.7	21	12	US-10-006-172A-105

C 17	14	0.7	21	12	US-10-015-392A-105	Sequence 105, App
C 18	14	0.7	21	12	US-10-017-253A-105	Sequence 105, App
C 19	14	0.7	21	12	US-10-017-306A-105	Sequence 105, App
C 20	14	0.7	21	12	US-10-012-064A-105	Sequence 105, App
C 21	14	0.7	21	12	US-10-017-867A-105	Sequence 105, App
C 22	14	0.7	21	12	US-10-012-101B-105	Sequence 105, App
C 23	14	0.7	21	12	US-10-012-137A-105	Sequence 105, App
C 24	14	0.7	21	12	US-10-012-752A-105	Sequence 105, App
C 25	14	0.7	21	12	US-10-012-753A-105	Sequence 105, App
C 26	14	0.7	21	12	US-10-013-909A-105	Sequence 105, App
C 27	14	0.7	21	12	US-10-013-910A-105	Sequence 105, App
C 28	14	0.7	21	12	US-10-013-911A-105	Sequence 105, App
C 29	14	0.7	21	12	US-10-013-912A-105	Sequence 105, App
C 30	14	0.7	21	12	US-10-015-610A-105	Sequence 105, App
C 31	14	0.7	21	12	US-10-015-653A-105	Sequence 105, App
C 32	14	0.7	21	12	US-10-015-671A-105	Sequence 105, App
C 33	14	0.7	21	12	US-10-012-237A-105	Sequence 105, App
C 34	14	0.7	21	12	US-10-013-908A-105	Sequence 105, App
C 35	14	0.7	21	12	US-10-015-389A-105	Sequence 105, App
C 36	14	0.7	21	12	US-10-015-480A-105	Sequence 105, App
C 37	14	0.7	21	12	US-10-015-715A-105	Sequence 105, App
C 38	14	0.7	21	12	US-10-012-753A-105	Sequence 105, App
C 39	14	0.7	21	12	US-10-015-385A-105	Sequence 105, App
C 40	14	0.7	21	12	US-10-007-236A-105	Sequence 105, App
C 41	14	0.7	21	12	US-10-015-389A-105	Sequence 105, App
C 42	14	0.7	21	12	US-10-013-915A-105	Sequence 105, App
C 43	14	0.7	21	12	US-10-015-394A-105	Sequence 105, App
C 44	14	0.7	21	12	US-10-015-519A-105	Sequence 105, App
C 45	14	0.7	21	14	US-10-006-856A-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-10-098-263B-111281/c
; Sequence 111281, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111281
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-111281

Query Match 0.8%; Score 17; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 648 TCATCGGACTTCACC 664
DB 24 TCATCGGACTTCACC 8

RESULT 2
US-10-098-263B-53235/c
; Sequence 53235, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 53235
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-53235

Query Match 0.8%; Score 16; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 CTGGTCTGGACTTTG 1703
|||
DB 23 CTGGTCTGGACTTTG 8

RESULT 3
US-10-098-263B-22077
; Sequence 22077, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 22077
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-22077

Query Match 0.7%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 847 GCAGAAGAAGCTCTT 861
|||
DB 11 GCAGAAGAAGCTCTT 25

RESULT 4
US-10-098-263B-39977
; Sequence 39977, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 39977
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-39977

Query Match 0.7%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 847 GCAGAAGAAGCTCTT 861

DB 4 GCAGAAGAAGCTCTT 18
|||

RESULT 5
US-10-098-263B-41699
; Sequence 41699, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 41699
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-41699

Query Match 0.7%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAGGACGGGCTTCGG 1749
|||
DB 3 CAGGACGGGCTTCGG 17

RESULT 6
US-10-098-263B-64985
; Sequence 64985, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 64985
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-64985

Query Match 0.7%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 847 GCAGAAGAAGCTCTT 861
|||
DB 6 GCAGAAGAAGCTCTT 20

RESULT 7
US-10-098-263B-101971
; Sequence 101971, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759

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; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 101971
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-2638-101971

Query Match      0.7%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      847 GCAGAGAGAGCTCTT 861
DB      7 GCAGAGAGAGCTCTT 21

RESULT 8
US-10-339-782-485/C
; Sequence 485, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-0001100S
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 485
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-485

Query Match      0.7%; Score 14; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1298 CCATTACAGAGA 1311
DB      16 CCATTACAGAGA 3

RESULT 9
US-10-061-269-23
; Sequence 23, Application US/10061269
; Publication No. US20030087416A1
; GENERAL INFORMATION:
; APPLICANT: Mattes, Ralf
; APPLICANT: Klein, Kathrin
; APPLICANT: Schiweck, Hubert
; APPLICANT: Kunz, Markwart
; APPLICANT: Munir, Mohammed
; TITLE OF INVENTION: Preparation of Acariogenic Sugar
; SUBSTITUTES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/061,269
; FILING DATE: 04-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/374,155
; FILING DATE: 22-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05638.0006-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-061-269-23

Query Match      0.7%; Score 14; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1205 TGGTGGAGAGAGC 1218
DB      1 TGGTGGAGAGAGC 14

RESULT 10
US-10-058-422-19/C
; Sequence 19, Application US/10058422
; Publication No. US20030108881A1
; GENERAL INFORMATION:
; APPLICANT: Hyeoung Lee, Hye Eun Bang, Sang-Nae Cho, Gill-Han Bai,
; APPLICANT: Sang-Jae Kim
; TITLE OF INVENTION: A method for identifying Micobacteria tuberculosis and
; TITLE OF INVENTION: non-tuberculosis Micobacteria, together with detecting resista
; TITLE OF INVENTION: to an antituberculosis drug of Micobacteria obtained by mutati
; TITLE OF INVENTION: of rpoB gene
; FILE REFERENCE: 0217-0008
; CURRENT APPLICATION NUMBER: US/10/058,422
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 19
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligomer probe for M. szulgai
US-10-058-422-19

Query Match      0.7%; Score 14; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1483 GCCGACGTTCCAGAT 1496
DB      16 GCCGACGTTCCAGAT 3

RESULT 11
US-10-215-271-15/C
; Sequence 15, Application US/10215271
; Publication No. US20030091547A1
; GENERAL INFORMATION:
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Edelberg, Jay M.

```


APPLICANT: Rafii, Shahin
APPLICANT: Hong, Mun K.
TITLE OF INVENTION: Platelet-Derived Growth Factor Protection of Cardiac Myocardium
FILE REFERENCE: 1676.003U51
CURRENT APPLICATION NUMBER: US/10/215,271
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: US 60/357,328
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/311,238
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 20
TYPE: DNA
ORGANISM: Mus musculus
US-10-215-271-15

Query Match 0.78; Score 14; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04; -
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1962 TGAGGAGGAGCAA 1875
|||||||
Db 18 TGAGGAGGAGCAA 5

RESULT 12
US-09-946-374-105/c
Sequence 105, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleon
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536

PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099808
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
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PRIOR FILING DATE: 1998-09-15
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PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100584
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100651
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100711
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101068
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101071
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101471
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101472
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101474
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23

;; PRIOR APPLICATION NUMBER: 60/101476
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101477
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101479
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101738
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101743
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101915
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101916
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/102207
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102240
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102307
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102330
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102331
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102484
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102487
;; PRIOR FILING DATE: 1998-09-30
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;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102571
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102684
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102687
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102965
;; PRIOR FILING DATE: 1998-10-02
;; PRIOR APPLICATION NUMBER: 60/103258
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103314
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103315
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103328
;; PRIOR FILING DATE: 1998-10-07
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;; PRIOR APPLICATION NUMBER: 60/103396
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;; PRIOR APPLICATION NUMBER: 60/103679
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103711
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/104257
;; PRIOR FILING DATE: 1998-10-14
;; PRIOR APPLICATION NUMBER: 60/104987
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104

;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807

Query Match 0.7%; Score 14; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1868 AGGAGCAACAGCAG 1881
Db 19 AGGAGCAACAGCAG 6

RESULT 13

US-10-015-387A-105/c
; Sequence 105, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015.387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-387A-105

Query Match 0.7%; Score 14; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1868 AGGAGCAACAGCAG 1881
Db 19 AGGAGCAACAGCAG 6

RESULT 14

US-10-227-596-5
; Sequence 5, Application US/10227596
; Publication No. US20030133910A1
; GENERAL INFORMATION:
; APPLICANT: You, Ming
; APPLICANT: Wang, Yian
; APPLICANT: Zhang, Zhongqiu
; TITLE OF INVENTION: Wild-type ras as a cancer therapeutic agent
; FILE REFERENCE: 22727/04100

; CURRENT APPLICATION NUMBER: US/10/227,596
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: US 60/314,693
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-227-596-5

Query Match 0.7%; Score 14; DB 12; Length 21;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1513 GTCAACGCTGAGAG 1526
|||||
Db 4 GTCAACGCTGAGAG 17

RESULT 15
US-10-006-130A-105/c
; Sequence 105 Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-130A-105

Query Match 0.7%; Score 14; DB 12; Length 21;
Best Local Similarity 100.0%; Pred.No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1868 AGGAGCAACGACGAG 1881
|||||
Db 19 AGGAGCAACGACGAG 6

Search completed: November 9, 2003, 04:35:24
Job time : 433 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: November 9, 2003, 04:21:18, Search time 2912 Seconds
(without alignments)
16892.946 Million cell updates/sec

Title: US-09-856-327-1_COPY_1_2024
Perfect score: 2024
Sequence: 1 atcagcatgtctctctca.....ttatggcaactatgattcatg 2024

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 0
Total number of hits satisfying chosen parameters: 32728

Minimum DB seq length: 15
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database: EST:

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: gb_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_pbg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	0.7	25	AZ864400	AZ864400 2M0173P24
2	13	0.6	27	CC179499	CC179499 SALK 0700
3	13	0.6	29	BQ590345	BQ590345 E012842-0
4	12	0.6	19	C01216	C01216 HUMGS000792

C	5	12	0.6	20	28	AZ651194
C	6	12	0.6	21	28	AZ307451
	7	12	0.6	21	28	AZ580960
	8	12	0.6	21	28	AZ580960
	9	12	0.6	21	28	AZ602152
	10	12	0.6	21	28	AZ956341
	11	12	0.6	22	28	AZ371960
C	12	12	0.6	22	28	AZ785029
C	13	12	0.6	23	28	AZ471912
C	14	12	0.6	24	9	AW247823
	15	12	0.6	24	28	AZ408805
	16	12	0.6	25	14	L32062
	17	12	0.6	25	28	AZ851170
	18	12	0.6	25	29	TA125H10P
	19	12	0.6	26	29	TA169C05Q
C	20	12	0.6	27	28	AZ766232
C	21	12	0.6	28	9	AI381812
C	22	12	0.6	28	9	AI573029
C	23	12	0.6	28	28	AZ412247
C	24	12	0.6	29	14	L32036
C	25	12	0.6	29	29	TA128C02P
	26	12	0.6	30	14	C20897
	27	12	0.6	30	28	AZ785790
C	28	12	0.6	30	28	BH909424
	29	11	0.5	17	9	AW246893
	30	11	0.5	19	28	AZ484303
C	31	11	0.5	19	28	AZ514386
C	32	11	0.5	19	28	AZ586377
C	33	11	0.5	19	28	AZ604234
C	34	11	0.5	19	28	AZ807034
C	35	11	0.5	19	28	AZ942806
	36	11	0.5	20	28	AZ308421
C	37	11	0.5	20	28	AZ338911
C	38	11	0.5	20	28	AZ339957
	39	11	0.5	20	28	AZ404785
C	40	11	0.5	20	28	AZ600911
C	41	11	0.5	20	28	AZ611227
C	42	11	0.5	20	28	AZ759840
C	43	11	0.5	20	28	AZ862111
C	44	11	0.5	21	28	AZ352290
	45	11	0.5	21	28	AZ643740

ALIGNMENTS

RESULT 1
AZ864400
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AZ864400 25 bp DNA linear GSS 21-FEB-2001
2M0173P24R Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0173P24 R, genomic survey sequence.
AZ864400
GSS.
GI:13063663
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0173 row: P column: 24
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0173P24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|9B|AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 5 c 5 g 5 t

Query Match 0.7%; Score 14; DB 28; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.8e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 TGAAGCTGGTCTAC 185
 |||||
 Db 8 TGAAGCTGGTCTAC 21

RESULT 2

CC179499/c
 LOCUS CCI179499 27 bp DNA linear GSS 02-MAY-2003
 DEFINITION SALK 070019.48.10.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_070019.48.10.x genomic survey sequence.

ACCESSION CCI179499
 VERSION CCI179499.1 GI:30318050
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 27)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished
 CONTACT: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752

COMMENT

FEATURES
 source
 1. .27
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 13 a 3 c 3 g 8 t

Query Match 0.6%; Score 13; DB 29; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.8e+05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TCTATGCAATCA 62
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 Db 24 TCTATGCAATCA 12

RESULT 3

BQ590345
 LOCUS BQ590345 29 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012842-024-019-D12-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
 CDNA clone 024-019-D12 5-PRIME, mRNA sequence.

ACCESSION BQ590345
 VERSION BQ590345.1 GI:26119928
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 29)

REFERENCE Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 29 Std Error: 0.00
 Plate: 19 row: 9 column: 12
 Seq primer: SP6; CATACGATTAGGTAGCAGCTATAG.

FEATURES
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 1. .29
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:189772"
 /db_xref="taxon:161934"
 /clone="024-019-D12"
 /tissue_type="storage root"
 /lab_host="EMDH108"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: PCMVSPORT6; Site_1: SalI; Site_2: NotI;

Fax: 858 558 6379
 Email: ecker@salk.edu.
 This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.

Location/Qualifiers
 1. .27
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 13 a 3 c 3 g 8 t

Query Match 0.6%; Score 13; DB 29; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.8e+05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 TCTATGCAATCA 62
 |||||
 Db 24 TCTATGCAATCA 12

RESULT 3
 BQ590345
 LOCUS BQ590345 29 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012842-024-019-D12-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
 CDNA clone 024-019-D12 5-PRIME, mRNA sequence.

ACCESSION BQ590345
 VERSION BQ590345.1 GI:26119928
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 29)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 29 Std Error: 0.00
 Plate: 19 row: 9 column: 12
 Seq primer: SP6; CATACGATTAGGTAGCAGCTATAG.

FEATURES
 source
 1. .29
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:189772"
 /db_xref="taxon:161934"
 /clone="024-019-D12"
 /tissue_type="storage root"
 /lab_host="EMDH108"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: PCMVSPORT6; Site_1: SalI; Site_2: NotI;

cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulze@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet project
local PI: Dr. Katharina Schneider, coordinator; Prof.
Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

BASE COUNT 9 a 2 c 7 g 11 t
ORIGIN
Query Match 0.6%; Score 13; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1960 TTGAAGATTTTG 1972
|||||
Db 5 TTGAAGATTTTG 17

RESULT 4
C01216/c
LOCUS
DEFINITION HUMGS0007928 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
sequence.
ACCSSION
VERSION C01216.1 GI:1433446
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Okubo.K.
BodyMap; human gene expression database
Unpublished
Contact: Okubo.K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see ' <http://www.imcb.osaka-u.ac.jp/bodymap>'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES
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1. .19
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/notes="One or more human adult tissues"
BASE COUNT 1 a 4 c 5 g 8 t 1 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1304 ACAGAAGACAC 1315
|||||
Db 18 ACAGAAGACAC 7

RESULT 5
AZ651194/c
LOCUS
DEFINITION IM0521F18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source

1. .20
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0521F18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 2. a 3 c 6 g 11 t
ORIGIN

Query Match 0.6%; Score 12; DB 28; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1289 GTAACACCCCA 1300
|||||
Db 16 GTAACACCCCA 5

RESULT 6
AZ307451/c
LOCUS
DEFINITION AZ307451 21 bp DNA linear GSS 29-SEP-2000

clone UUGC1M0521F18 R, genomic survey sequence.
AZ651194
VERSION
AZ651194.1 GI:11786441
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn.D., Aoyagi.A., Barber.M., Beacorn.T., Duval.B., Hamil.C.,
Islam.H., Longacre.S., Mahmoud.M., Meenen.E., Pedersen.T., Reilly
M., Rose.M., Rose.R., Stokes.R., Tingey.A., von Niederhausern.A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0521 row: F column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

DEFINITION IM0009E09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0009E09 F, genomic survey sequence.

ACCESSION AZ307451

VERSION AZ307451.1 GI:10346464

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

UNPUBLISHED

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH GENOME CENTER

RM. 308, BIOMEDICAL POLYMERS RESEARCH BLDG., 20 S. 2030 E., SLC, UT 84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

INSERT LENGTH: 10000 STD ERROR: 0.00

PLATE: 0009 ROW: 2 COLUMN: 09

SEQ PRIMER: CGTGTAAACGACGGCCAGT

CLASS: plasmid ends

HIGH QUALITY SEQUENCE STOP: 21.

LOCATION/QUALIFIERS

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0009E09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 8 c 6 g 2 t

ORIGIN

Query Match 0.6%; Score 12; DB 28; Length 21;

Best Local Similarity 100.0%; Pred. No. 5.9e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1740 CGGGCTTCGGCG 1751

Db 15 CGGGCTTCGGCG 4

RESULT 7

AZ580960

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

UNPUBLISHED

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH GENOME CENTER

RM. 308, BIOMEDICAL POLYMERS RESEARCH BLDG., 20 S. 2030 E., SLC, UT 84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

INSERT LENGTH: 10000 STD ERROR: 0.00

PLATE: 0369 ROW: P COLUMN: 04

SEQ PRIMER: CACACAGAAACAGCTATGACC

CLASS: plasmid ends

HIGH QUALITY SEQUENCE STOP: 21.

LOCATION/QUALIFIERS

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0369F04"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 9 c 2 g 8 t

ORIGIN

Query Match 0.6%; Score 12; DB 28; Length 21;

Best Local Similarity 100.0%; Pred. No. 5.9e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 CACCTTGTCT 702

Db 8 CACCTTGTCT 19

RESULT 8

AZ580960

AZ602152
LOCUS 21 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0420H13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0420H13 R, genomic survey sequence.
ACCESSION AZ602152
VERSION AZ602152.1 GI:11724342
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0420 row: H column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
2 a 2 c 3 g 14 t

BASE COUNT
ORIGIN

Query Match 0.6%; Score 12; DB 28; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1967 ATTTCGTGATT 1978
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DB 8 ATTTCGTGATT 19

RESULT 9
AZ956341
LOCUS 21 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0222H16R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0222H16 R, genomic survey sequence.
ACCESSION AZ956341
VERSION AZ956341.1 GI:13827568
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 row: H column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21

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/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
8 a 3 c 2 g 8 t

BASE COUNT
ORIGIN

Query Match 0.6%; Score 12; DB 28; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1973 TGTATTACTGAA 1984
|||||
DB 4 TGTATTACTGAA 15

RESULT 10
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 LOCUS
 DEFINITION
 1M0123C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0123C10 R, genomic survey sequence.

ACCESSION
 AZ371960
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0123 row: C column: 10
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 6 a 2 c 3 g 11 t

Query Match 0.6%; Score 12; DB 28; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.9e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TGAATGATTCAT 126
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 Db 11 TGAATGATTCAT 22

RESULT 11
 AZ785029
 LOCUS
 DEFINITION
 2M0028101R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0028101 R, genomic survey sequence.

ACCESSION
 AZ785029
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0028 row: I column: 01
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0028101"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 3 a 8 c 4 g 7 t

Query Match 0.6%; Score 12; DB 28; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.9e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1257 TGCCCATTCGGT 1268
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Db          5 TGCCCATTCGGT 16

RESULT 12
LOCUS      AZ471912/c
DEFINITION 1M0286K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0286K14 R, genomic survey sequence.
ACCESSION  AZ471912
VERSION     AZ471912.1 GI:10630037
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT     Contact: Robert B Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunne@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0286 row: K column: 14
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
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                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
            4 a 1 c 13 g 5 t

BASE COUNT 0.6%; Score 12; DB 28; Length 23;
ORIGIN      Best Local Similarity 100.0%; Pred. No. 6e+05;
            Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
1277 CCGGACCCCG 1288
|||||
Db          24 CCGGACCCCG 13

RESULT 14

Db          18 ACACTTGATCCC 7

RESULT 13
LOCUS      AW247823/c
DEFINITION 2820397.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820397 3',
            mRNA sequence.
ACCESSION  AW247823
VERSION     AW247823.1 GI:6590816
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 24)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Other ESTs: 2820397.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: c9apbs@remail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LNL at:
            www-bio.lnl.gov/bbrp/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 19
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 24 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LICM4 row: B column: 14
            High quality sequence stop: 19.
            Location/Qualifiers
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                /db_xref="taxon:9606"
                /clone="IMAGE:2820397"
                /tissue_type="small cell carcinoma"
                /cell_line="MGC3"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_7"
                /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5',
            adaptor: GGACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
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AZ408805
LOCUS 24 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0180801F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0180801 F, genomic survey sequence.
ACCESSION AZ408805
VERSION AZ408805.1 GI:10532818
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: B column: 01
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

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1..24
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/clone="UUGC1M0180801"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 7 c 5 g 8 t
ORIGIN

Query Match 0.6%; Score 12; DB 28; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1433 AACCTTTGGTT 1444
|||||
Db 4 AACCTTTGGTT 15

RESULT 15

L32062
LOCUS 25 bp mRNA linear EST 08-JUN-1995
DEFINITION HUMXP9F3A Human placenta Homo sapiens cDNA clone XP9F3A, mRNA sequence.
ACCESSION L32062
VERSION L32062.1 GI:927100
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 25)
AUTHORS Lee, C.-C., Yazdani, A., Wehnert, M., Bailey, J., Couch, L., Xiong, M., Coolbaugh, M.I., Chinnault, C.A., Baldini, A., Lindsay, E.A., Zhao, Z.-Y. and Caskey, C.T.H.
TITLE Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries
JOURNAL Hum. Mol. Genet. 4, 1373-1380 (1995)
MEDLINE 96090257
PUBMED 7581376
COMMENT Contact: Caskey, C.T.H.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="Xq13"
/clone="XP9F3A"
/clone_lib="Human placenta"
/note="Arrayed cDNAs and cosmid libraries from human placental tissue"

BASE COUNT

5 a 3 c 10 g 7 t
ORIGIN

Query Match 0.6%; Score 12; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 GATGACACGACG 850
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Db 14 GATGACACGACG 25
|||||

Search completed: November 9, 2003, 06:49:46
Job time : 2916 secs

? 14/3/1-17

4/3/1 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2002 American Chemical Society. All rts. reserv.

136227517 CA: 136(15)227517z JOURNAL
A transformation system for an ectomycorrhizal basidiomycete, *Lyophyllum*
shimeji

AUTHOR(S): Saito, Takeshi; Tanaka, Norio; Shinozawa, Takao
LOCATION: Department of Biological and Chemical Engineering, Faculty of
Engineering, Gunma University, Gunma, Japan, 376-8515
JOURNAL: Biosci., Biotechnol., Biochem. DATE: 2001 VOLUME: 65 NUMBER:
8 PAGES: 1928-1931 CODEN: BBIEJ ISSN: 0916-8451 LANGUAGE: English
PUBLISHER: Japan Society for Bioscience, Biotechnology, and Agrochemistry

4/3/2 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2002 American Chemical Society. All rts. reserv.

136017756 CA: 136(21)7756a JOURNAL
First Simultaneous Isolation of a Ribosome Inactivating Protein and an
Antifungal Protein from a Mushroom (*Lyophyllum shimeji*) Together with
Evidence for Synergism of their Antifungal Effects
AUTHOR(S): Lam, S. K.; Ng, T. B.
LOCATION: Department of Biochemistry, Faculty of Medicine, The Chinese
University of Hong Kong, Shatin, Hong Kong, Peop. Rep. China,
JOURNAL: Arch. Biochem. Biophys. DATE: 2001 VOLUME: 393 NUMBER: 2
PAGES: 271-280 CODEN: ABBA4 ISSN: 0003-9861 LANGUAGE: English
PUBLISHER: Academic Press

4/3/3 (Item 3 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2002 American Chemical Society. All rts. reserv.

135268257 CA: 135(19)268257n PATENT
Fruit-body formation gene of mushroom *Pleurotus ostreatus*
INVENTOR(AUTHOR): Iwata, Masato; Fujii, Takao
LOCATION: Japan,
ASSIGNEE: I.M.B. K. K.
PATENT: Japan Kokai Tokkyo Koho: JP 2001258567 A2 DATE: 20010925
APPLICATION: JP 200079173 (20000321)
PAGES: 15 pp. CODEN: JKOXAF LANGUAGE: Japanese CLASS: C12N-015/09A;
A01H-005/008; C12N-001/158; C12N-015/098; C12N-001/645B

4/3/4 (Item 4 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
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135030442 CA: 135(3)30442u JOURNAL
Screening of a unique lectin from 16 cultivable mushrooms with hybrid
glycoprotein and neoproteoglycan probes and purification of a novel

N-acetylglucosamine-specific lectin from *Oudemansiella platyphylla* fruiting
body

AUTHOR(S): Matsumoto, H.; Natsume, A.; Ueda, H.; Saitoh, T.; Ogawa, H.
LOCATION: Graduate School of Humanities and Sciences, Course of Advanced
Biosciences, Ochanomizu University, Bunkyo-ku, Tokyo, Japan, 112-8610
JOURNAL: Biochim. Biophys. Acta DATE: 2001 VOLUME: 1526 NUMBER: 1
PAGES: 37-43 CODEN: BBACAQ ISSN: 0006-3002 PUBLISHER ITEM IDENTIFIER:
0304-4165(01)00094-0 LANGUAGE: English PUBLISHER: Elsevier Science B.V.

4/3/5 (Item 5 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
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134247999 CA: 134(18)247999v PATENT
Lyophyllum shimeji antibacterial protein with pyranose oxidase activity
INVENTOR(AUTHOR): Takakura, Yoshimitsu; Kuwata, Shigeru; Inoue, Yasuhiro
LOCATION: Japan,
ASSIGNEE: Japan Tobacco Inc.; Corporate Juridical Person, Society for
Techno-Innovation of Agriculture, Fo
PATENT: PCT International: WO 200121657 A1 DATE: 20010329
APPLICATION: WO 2000JP6404 (20000920) *JP 99267238 (19990921)
PAGES: 52 pp. CODEN: PIXX02 LANGUAGE: Japanese CLASS: C07K-014/375A;
C12N-015/318; C12N-015/638; C12N-001/218; C12Q-001/688; C12P-021/028;
A01N-065/008 DESIGNATED COUNTRIES: AU; CA; CN; JP; KR; US
DESIGNATED REGIONAL: AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT;
LU; MC; NL; PT; SE

4/3/6 (Item 6 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
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133233430 CA: 133(17)233430v JOURNAL
Cloning and sequence analysis of the glyceraldehyde-3-phosphate
dehydrogenase gene from the ectomycorrhizal basidiomycete *Lyophyllum*
shimeji

AUTHOR(S): Saito, Takeshi; Tanaka, Norio
LOCATION: The Mushroom Research Institute of Japan, Gunma, Japan,
376-0051
JOURNAL: Mycoscience DATE: 1999 VOLUME: 40 NUMBER: 6 PAGES: 517-523
CODEN: MNCEED ISSN: 1340-3540 LANGUAGE: English PUBLISHER: Mycological
Society of Japan

4/3/7 (Item 7 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
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131014873 CA: 131(2)14873x PATENT
Cloning of promoter and terminator of gene for glyceraldehyde-3-phosphate
dehydrogenase of *Lyophyllum shimeji* for preparation of vectors
INVENTOR(AUTHOR): Saito, Takeshi
LOCATION: Japan,
ASSIGNEE: Mori Sangyo K. K.

applicant

Reviews!

PATENT: Japan Kokai Tokkyo Koho : JP 99127863 A2 ; JP 11127863 DATE: 19990518
APPLICATION: JP 97301078 (19971031)
PAGES: 9 pp. CODEN: JKOXAF LANGUAGE: Japanese CLASS: C12N-015/09A; C12N-001/15B; C12N-015/09B; C12N-001/645B

4/3/8 (Item 8 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
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128292615 CA: 128(24)292615d JOURNAL
Culture conditions for commercial production of *Lyophyllum shimeji*
AUTHOR(S): Ohta, Akira
LOCATION: Shiga For. Res. Cent., Shiga, Japan, 520-2321
JOURNAL: Nippon Kingakkaï Kaïho DATE: 1998 VOLUME: 39 NUMBER: 1
PAGES: 13-20 CODEN: NKKEH ISSN: 0029-0289 LANGUAGE: Japanese
PUBLISHER: Nippon Kingakkaï

4/3/9 (Item 9 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
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121053711 CA: 121(5)53711f JOURNAL
Systematics of *Lyophyllum* section *Difformia* based on evidence from
culture studies and ribosomal DNA sequences
AUTHOR(S): Moncalvo, Jean Marc; Rehner, Stephen A.; Vilgalys, Rytas
LOCATION: Inst. Systematic Bot., Univ. Lausanne, CH-1015, Lausanne,
Switz.
JOURNAL: Mycologia DATE: 1993 VOLUME: 85 NUMBER: 5 PAGES: 788-94
CODEN: MYCOAE ISSN: 0027-5514 LANGUAGE: English

4/3/10 (Item 1 from file: 50)
DIALOG(R)File 50:CAB Abstracts
(c) 2002 CAB International. All rts. reserv.

03817933 CAB Accession Number: 990613196
Comparison of mycorrhizal fungi associated with *Pinus* species in
cultural characteristics, and artificial mycorrhizal synthesis on *Pinus*
thunbergii seedlings.
Lee Jongkyu; Lee HoonYong; Lee SangYong
Forest Resources Protection, Division of Forest Resources, College of
Forest Sciences, Kangwon National University, 200-701, Korea Republic.
Journal of Forest Science - Kangwon National University vol. 15 p.77-88
Publication Year: 1999 ..
Language: Korean Summary Language: english
Document Type: Journal article

4/3/11 (Item 1 from file: 94)
DIALOG(R)File 94:JICST-EPlus
(c)2002 Japan Science and Tech Corp(JST). All rts. reserv.

04967094 JICST ACCESSION NUMBER: 01A0876250 FILE SEGMENT: JICST-E
Properties of Monokaryotic Hyphae and Mating System of *Lyophyllum*
shimeji.

KAWAI MASATAKA (1)
(1) Narakenshinringise
Naraken Shinrin Gijutsu Senta Kenkyu Hokou(Bulletin of the Nara Forest
Research Institute), 2000, NO.30, PAGE.17-20, TBL.2, REF.7
JOURNAL NUMBER: 207044CA ISSN NO: 1345-9864
UNIVERSAL DECIMAL CLASSIFICATION: 635.17.8
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Original paper
MEDIA TYPE: Printed Publication

4/3/12 (Item 2 from file: 94)
DIALOG(R)File 94:JICST-EPlus
(c)2002 Japan Science and Tech Corp(JST). All rts. reserv.

03317070 JICST ACCESSION NUMBER: 98A0636276 FILE SEGMENT: PreJICST-E
Sequence analysis of the GPD gene from *Lyophyllum shimeji*
and construction of a vector with the transcriptional control regions
for transformation of mushrooms.
SAITO TAKESHI (1); KAWAI GENSHIRO (1)
(1) Mori & Co., Ltd.
Nippon Kin Gakkai Taikai Koen Yoshishu(Proceedings of the Annual Meeting of
the Mycological Society of Japan. Abstracts of Submitted Papers), 1998
VOL.42nd, PAGE.67
JOURNAL NUMBER: X0656AAM
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Conference Proceeding
MEDIA TYPE: Printed Publication

4/3/13 (Item 3 from file: 94)
DIALOG(R)File 94:JICST-EPlus
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01772930 JICST ACCESSION NUMBER: 93A0410149 FILE SEGMENT: JICST-E
Inoculation of Symbiotic Mushroom Fungi to In vitro Cultured Japanese Black
Pine (*Pinus thunbergii*) and Japanese Red Oak (*Quercus acutissima*).
ISHII KATSUAKI (1); ODANI KEIJI (1); WASE KOJI (2); OGAWA MAKOTO (2)
(1) Shinninsoken; (2) Kansaihogokankyose
Shokubutsu Soshiki Baiyo(Plant Tissue Culture Letters), 1993, VOL.10, NO.1,
PAGE.84-88, FIG.2, TBL.5, REF.6
JOURNAL NUMBER: L0316AAJ ISSN NO: 0289-5773 CODEN: SSB AE
UNIVERSAL DECIMAL CLASSIFICATION: 630*12
LANGUAGE: Japanese COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Short Communication
MEDIA TYPE: Printed Publication

4/3/14 (Item 4 from file: 94)
DIALOG(R)File 94:JICST-EPlus

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01575072 JICST ACCESSION NUMBER: 92A0451580 FILE SEGMENT: JICST-E
A comparative study of fruit body morphology and culture characters in the
Lyophyllum decastes complex (Agaricales, Basidiomycetes) from
Japan and Europe.

MONGALYO J M (1); CLEMENCON H (1)
(1) Univ. Lausanne, Lausanne, CHE
Trans Mycol Soc Jpn, 1992, VOL.33, NO.1, PAGE.3-11, FIG.2, TBL.1, REF.9
JOURNAL NUMBER: X0034AAC ISSN NO: 0029-0289
UNIVERSAL DECIMAL CLASSIFICATION: 579.23+579.8
LANGUAGE: English COUNTRY OF PUBLICATION: Japan
DOCUMENT TYPE: Journal
ARTICLE TYPE: Original paper
MEDIA TYPE: Printed Publication

4/3/15 (Item 1 from file: 71)

DIALOG(R)File 71:ELSEVIER BIOBASE

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01889551 2001251487

Isolation of pleurotigin, a novel ribosome-inactivating protein from fresh
sclerotia of the edible mushroom pleurotus tuber-regium

Wang H.X.; Ng T.B.

ADDRESS: T.B. Ng, Department of Biochemistry, Faculty of Medicine, Chinese
University of Hong Kong, Shatin, New Territories, Hong Kong
EMAIL: biochemistry@cuhk.edu.hk

Journal: Biochemical and Biophysical Research Communications, 288/3
(718-721), 2001, United States

PUBLICATION DATE: November 2, 2001

CODEN: BBRCA

ISSN: 0006-291X

DOCUMENT TYPE: Article

LANGUAGES: English SUMMARY LANGUAGES: English

NO. OF REFERENCES: 23

4/3/16 (Item 1 from file: 73)

DIALOG(R)File 73:EMBASE

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11465747 EMBASE No: 2002037213

Screening of edible Japanese plants for suppressive effects on phorbol
ester-induced superoxide generation in differentiated HL-60 cells and
A552 cells

Ha W.K.; Murakami A.; Nakamura Y.; Ohigashi H.

H. Ohigashi, Division of Food Science, Graduate School of Agriculture,
Kyoto University, Kyoto 606-8502 Japan

AUTHOR EMAIL: ohigashi@kais.kyoto-u.ac.jp

Cancer Letters (CANCER LETT.) (Ireland) 08 FEB 2002, 176/1 (7-16)

CODEN: CALED ISSN: 0304-3835

PUBLISHER ITEM IDENTIFIER: S0304383501007352

DOCUMENT TYPE: Journal ; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 36

4/3/17 (Item 1 from file: 285)

DIALOG(R)File 285:BioBusiness(R)

(c) 1998 BIOSIS. All rts. reserv.

00303554

Marked formation of thiazolidine-4-carboxylic acid, an effective nitrite
trapping agent in vivo, on boiling of dried shiitake mushroom (Lentinus
edodes).

Kurashima Y.; Tsuda M.; Sugimura T.

BIOCHEM. DIV., NATL. CANCER CENT. RES. INST., 1-1 TSUKUJI 5-CHOME, CHUO-KU,
TOKYO 104, JPN.

Journal of Agricultural and Food Chemistry Vol.38, No.10, p.1945-1949,
1990.

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